Basic Local Alignment Search Tool

NCBI/ BLAST/ blastp suite-2sequences/ Formatting Results - NBR3PYEF112

Blast 2 sequences

alignment of GenBank Prot ID 3193318 and claimed SEQ ID NO: 2

Query ID <u>gi[10177290|dbi[BAB10551.1]</u>

Description unnamed protein product

[Arabidopsis thaliana]

Molecule type amino acid

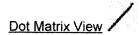
Query Length 186

Subject ID 32133

Description None **Molecule type** amino acid

Subject Length 228

Program BLASTP 2.2.25+



Plot of gi|10177290|dbj|BAB10551.1| vs 32133 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer 2 PubChem BioAssay

Accession Description Max score Total score Query coverage E value Links

32133 unnamed protein product 127 127 84% 1e-34

Alignments

>lcl|32133 unnamed protein product Length=228

Score = 127 bits (319), Expect = 1e-34, Method: Compositional matrix adjust. Identities = 78/167 (47%), Positives = 96/167 (58%), Gaps = 11/167 (6%)

Query 14 ACKFLRRKCMPGCIFAPYFPPEE-PHKFANVHKIFGASNVTKLLNELLPHQREDAVNSLA 72 ACKFLRRKC+ GCIFAPYF E+ FA VHK+FGASNV+KLL+ + H+R DAV S+

Sbjct 20 ACKFLRRKCVAGCIFAPYFDSEQGAAHFAAVHKVFGASNVSKLLHHVPEHKRPDAVVSIC 79

Query 73 YEAEARVRDPVYGCVGAISYLQRQVHRLQKELDAANADLAHYGLSTSAAGAPGNVVDLVF 13:

Query 73 YEAEARVRDPVYGCVGAISYLQRQVHRLQKELDAANADLAHYGLSTSAAGAPGNVVDLVF 132 +EA+AR+RDP+YGCV I LQ+QV LQ EL A LA L Sbjct 80 FEAQARLRDPIYGCVSHIVSLQQQVVSLQTELSYLQAHLATLELPQPQPPPQVPVSSSGSL 139

Query 133 QPQPLPSQQLPPLNP-VYRLSGA-SPVMN-----QMPRGTGGSYGT 171

Q L LP ++P VY LS PVM+ Q PR + +G Sbjct 140 --QALSITDLPTISPSVYDLSSIFEPVMSSTWAMQQQPRPSDHLFGV 184